

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 18, 2001, 04:27:57 ; Search time 44.79 Seconds
(without alignments)
152.348 Million cell updates/sec

Title: US-09-090-867-2
Perfect score: 2104
Sequence: 1 MAFVCLAIICLTFTFLSTF.....LLLRKNTYPMKMPFCODI 380

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA.*
1: /cgn1_7/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn1_7/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn1_7/ptodata/1/1aa/6.COMB.pep.*
4: /cgn1_7/ptodata/1/1aa/PCITUS.COMB.pep.*
5: /cgn1_7/ptodata/1/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2104	100.0	380	1	US-08-609-572-4
2	1194.5	56.8	383	1	US-08-609-572-2
3	111.5	14.8	420	1	US-07-757-390-13
4	111.5	14.8	420	1	US-08-442-282-13
5	111.5	14.8	420	1	US-08-442-281-13
6	111.5	14.8	420	2	US-08-939-727-13
7	111.5	14.8	396	1	US-07-757-390-14
8	310.5	14.8	396	1	US-08-442-282-14
9	310.5	14.8	396	1	US-08-442-281-14
10	310.5	14.8	396	2	US-08-939-727-14
11	295.5	14.0	427	3	US-08-969-125-9
12	293	13.9	313	3	US-08-836-561-106
13	292	13.9	335	1	US-07-947-130-2
14	292	13.9	335	1	US-08-421-823-2
15	292	13.9	335	1	US-08-421-823-2
16	247	11.7	398	1	US-07-757-390-6
17	247	11.7	398	1	US-08-442-282-6
18	247	11.7	398	1	US-08-442-281-6
19	247	11.7	398	2	US-08-939-727-6
20	247	11.7	415	1	US-07-757-390-5
21	247	11.7	415	1	US-08-442-282-5
22	247	11.7	415	1	US-08-442-281-5
23	247	11.7	415	2	US-08-939-727-5
24	229	10.9	315	1	US-07-757-390-8
25	229	10.9	315	1	US-08-442-282-8
26	229	10.9	315	1	US-08-442-281-8
27	229	10.9	315	2	US-08-939-727-8
28	229	10.9	332	1	US-07-757-390-7

29	229	10.9	332	1	US-08-442-282-7	Sequence 7, Appl1
30	229	10.9	332	1	US-08-442-281-7	Sequence 7, Appl1
31	229	10.9	332	2	US-08-939-727-7	Sequence 7, Appl1
32	229	10.9	335	1	US-07-947-130-3	Sequence 3, Appl1
33	229	10.9	335	1	US-08-421-822-3	Sequence 3, Appl1
34	229	10.9	335	1	US-08-421-823-3	Sequence 3, Appl1
35	220	10.5	369	1	US-08-052-205-4	Sequence 4, Appl1
36	220	10.5	369	1	US-08-595-974-4	Sequence 4, Appl1
37	219	10.4	347	1	US-08-052-205-7	Sequence 7, Appl1
38	219	10.4	347	1	US-08-595-974-7	Sequence 7, Appl1
39	212.5	10.1	369	2	US-08-424-224-2	Sequence 2, Appl1
40	212.5	10.1	369	4	PCT-US94-02891-69	Sequence 69, Appl1
41	207	9.8	252	1	US-08-052-205-9	Sequence 9, Appl1
42	207	9.8	252	1	US-08-595-974-9	Sequence 9, Appl1
43	206	9.8	230	1	US-08-052-205-11	Sequence 11, Appl1
44	206	9.8	230	1	US-08-595-974-11	Sequence 11, Appl1
45	180.5	8.6	897	1	US-07-960-389-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-609-572-4
Sequence 4, Application US/08609572
Patent No. 5710023

ay
Seq ID No 2

GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Filiz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,572
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-572-4

Query Match 100.0% Score 2104; DB 1; Length 380;
Best Local Similarity 100.0% Pred. No. 3.6e-208;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MAFVCLAIICLTFTFLSTFGCTSSSDTEIKVNPDDFEIVDGVYVYVLAQNPPLSD 60
|||||

Db 1 MAVFVLAIGLTYFLISTTGTCTSSDTEIKVNPPODFEIVDPGLGYLYLOMQLPLSLD 60
 QY 61 HRECTVEYELKRNIGSETWKTITRNLYKDGFDLNGIEAKIHTLLPMQCTNSSEVQ 120
 Db 61 HRECTVEYELKRNIGSETWKTITRNLYKDGFDLNGIEAKIHTLLPMQCTNSSEVQ 120
 QY 121 SSAEFTYWSPGIPEPTKQVDMDCVYNNQYLLCSKRPBGIGVLLDTNLYLFYEGLDH 180
 Db 121 SSAEFTYWSPGIPEPTKQVDMDCVYNNQYLLCSKRPBGIGVLLDTNLYLFYEGLDH 180
 QY 181 ALQCVYIKADGONICRPFYLEASDYKDYICVNGSSEKPIRSSYFFOLQNIYKPLP 240
 Db 181 ALQCVYIKADGONICRPFYLEASDYKDYICVNGSSEKPIRSSYFFOLQNIYKPLP 240
 QY 241 PVLFTFRESSCEIKLWSIPLGPAPCFDYEIEIREDDTTLVTATVENEYTLTKTNE 300
 Db 241 PVLFTFRESSCEIKLWSIPLGPAPCFDYEIEIREDDTTLVTATVENEYTLTKTNE 300
 QY 301 TROLCEVVRKVNIVCSDDGIMSEMSDKOCWEGEDLSKTLRFWLPFGFILLVIFVTG 360
 Db 301 TROLCEVVRKVNIVCSDDGIMSEMSDKOCWEGEDLSKTLRFWLPFGFILLVIFVTG 360
 QY 361 LLLRKPTYPKMIPEFCDF 380
 Db 361 LLLRKPTYPKMIPEFCDF 380

RESULT 2
 US-08-609-572-2
 : Sequence 2, Application US/08609572
 : Patent No. 5710023

GENERAL INFORMATION:
 APPLICANT: Collins, Mary
 APPLICANT: Donaldson, Debra
 APPLICANT: Flitz, Lori
 APPLICANT: Neben, Tamlyn
 APPLICANT: Whiters, Matthew
 APPLICANT: Wood, Clive
 TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 Cambridge Park Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02140

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609/572
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 REFERENCE/DOCKET NUMBER: G15268
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8724
 TELEFAX: (617) 876-5891
 INFORMATION FOR SEQ ID NO. 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 383 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-609-572-2

Query Match

56.8%; Score 1194.5; DB 1; Length 383;

Best Local Similarity 58.9%; Pred. No. 1,2e-114;
 Matches 219; Conservative 55; Mismatches 91; Indels 7; Gaps 3;
 QY 1 MAVFVLAIGLTYFLISTTGTCTSSDTEIKVNPPODFEIVDPGLGYLYLOMQLPLSLD 60
 Db 1 MAVFVLAIGLTYFLISTTGTCTSSDTEIKVNPPODFEIVDPGLGYLYLOMQLPLSLD 60
 QY 61 HRECTVEYELKRNIGSETWKTITRNLYKDGFDLNGIEAKIHTLLPMQCTNSSEVQ 120
 Db 61 HRECTVEYELKRNIGSETWKTITRNLYKDGFDLNGIEAKIHTLLPMQCTNSSEVQ 120
 QY 121 SSAEFTYWSPGIPEPTKQVDMDCVYNNQYLLCSKRPBGIGVLLDTNLYLFYEGLDH 180
 Db 121 SSAEFTYWSPGIPEPTKQVDMDCVYNNQYLLCSKRPBGIGVLLDTNLYLFYEGLDH 180
 QY 181 ALQCVYIKADGONICRPFYLEASDYKDYICVNGSSEKPIRSSYFFOLQNIYKPLP 240
 Db 181 ALQCVYIKADGONICRPFYLEASDYKDYICVNGSSEKPIRSSYFFOLQNIYKPLP 240
 QY 241 PVLFTFRESSCEIKLWSIPLGPAPCFDYEIEIREDDTTLVTATVENEYTLTKTNE 300
 Db 241 PVLFTFRESSCEIKLWSIPLGPAPCFDYEIEIREDDTTLVTATVENEYTLTKTNE 300
 QY 301 TROLCEVVRKVNIVCSDDGIMSEMSDKOCWEGEDLSKTLRFWLPFGFILLVIFVTG 360
 Db 301 TROLCEVVRKVNIVCSDDGIMSEMSDKOCWEGEDLSKTLRFWLPFGFILLVIFVTG 360
 QY 361 LLLRKPTYPKMIPEFCDF 380
 Db 361 LLLRKPTYPKMIPEFCDF 380

RESULT 3
 US-07-757-390-13
 : Sequence 13, Application US/0757390
 : Patent No. 5453491

GENERAL INFORMATION:
 APPLICANT: Takatsu, Kiyoshi
 APPLICANT: Tomimaga, Akira
 APPLICANT: Takagi, Satoshi
 APPLICANT: Murata, Yoshiyuki
 TITLE OF INVENTION: Human And Murine Interleukin-5 Receptor
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penning & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/757/390
 FILING DATE: 19910910
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Mastrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7005-030
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 8698864/9741
 INFORMATION FOR SEQ ID NO. 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 420 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: unknown
 TOPOLOGY: linear

Thu Apr 19 08:07:46 2001

us-09-090-867-1.rni

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2001, 22:51:41 ; Search time 54.42 Seconds
(Without alignments) 3817.266 Million cell updates/sec

Title: US-09-090-867-1

Perfect score: 1289
Sequence: 1 CCCCCCCCCCGGAGAGAGAGG.....ACTGAATTTTCTTGGAA 1289

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn1_7/ptodata/1/lna/5A.COMB.seq:*
- 2: /cgn1_7/ptodata/1/lna/5B.COMB.seq:*
- 3: /cgn1_7/ptodata/1/lna/6.COMB.seq:*
- 4: /cgn1_7/ptodata/1/lna/PTUS.COMB.seq:*
- 5: /cgn1_7/ptodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1281	99.4	1369	1	US-08-609-572-3
2	610.4	47.4	1525	1	US-08-609-572-1
3	39.8	3.1	7218	1	US-08-233-463-14
4	37.6	2.9	10409	3	US-08-772-440-33
5	36.2	2.8	28604	3	US-08-781-891-207
6	35.8	2.8	2319	3	US-09-049-475-5
7	34.6	2.7	3507	1	US-08-315-468-3
8	34.4	2.7	4038	3	US-08-969-125-8
9	34.2	2.7	2686	3	US-09-358-384-1
10	34.2	2.7	3182	1	US-07-797-556-5
11	34.2	2.7	3182	1	US-07-943-843-1
12	34.2	2.7	3182	1	US-08-347-003-1
13	34.2	2.7	3591	1	US-07-943-843-5
14	34.2	2.7	3591	1	US-08-347-003-5
15	34	2.6	2258	1	US-07-720-589-1
16	34	2.6	2258	2	US-08-785-190-1
17	34	2.6	2258	4	PCT-US92-05539-1
18	34	2.6	7470	3	US-08-417-089-5
19	34	2.6	7470	3	US-08-619-651-5
20	33.2	2.6	885	3	US-08-952-089A-2
21	33.2	2.6	1588	3	US-08-952-089A-26
22	33.2	2.6	4146	3	US-08-952-089A-29
23	33	2.6	15331	3	US-09-128-155-16
24	32.6	2.5	1584	3	US-08-747-221B-51
25	32.6	2.5	1584	3	US-08-747-221B-52
26	32.6	2.5	2007	3	US-08-747-221B-36
27	32.6	2.5	2007	3	US-08-747-221B-38
28	32.2	2.5	405	3	US-08-806-597A-7

29	32.2	2.5	405	3	US-08-970-428A-7	Sequence 7, Appl1
30	32.2	2.5	1050	3	US-08-806-597A-13	Sequence 13, Appl1
31	32.2	2.5	1050	3	US-08-970-428A-13	Sequence 13, Appl1
32	32.2	2.5	4526	1	US-07-855-412B-4	Sequence 4, Appl1
33	32.2	2.5	4526	2	US-08-308-887A-4	Sequence 4, Appl1
34	32.2	2.5	4526	2	US-08-881-094-4	Sequence 4, Appl1
35	32	2.5	1002	1	US-08-243-543A-1	Sequence 1, Appl1
36	32	2.5	1188	1	US-07-757-390-11	Sequence 1, Appl1
37	32	2.5	1188	1	US-08-442-282-11	Sequence 1, Appl1
38	32	2.5	1188	1	US-08-442-282-11	Sequence 1, Appl1
39	32	2.5	1188	2	US-08-939-727-11	Sequence 11, Appl1
40	32	2.5	1260	1	US-07-757-390-9	Sequence 9, Appl1
41	32	2.5	1260	1	US-08-442-282-9	Sequence 9, Appl1
42	32	2.5	1260	1	US-08-442-281-9	Sequence 9, Appl1
43	32	2.5	1260	2	US-08-939-727-9	Sequence 9, Appl1
44	32	2.5	1998	3	US-09-280-759-195	Sequence 195, App
45	32	2.5	2006	1	US-07-757-390-10	Sequence 10, Appl1

ALIGNMENTS

Qy = seq ID No:1

RESULT 1
US-08-609-572-3
Sequence 3 Application US/08609572
Patent No. 5710023
GENERAL INFORMATION:
APPLICANT: Collins, Mary
APPLICANT: Donaldson, Debra
APPLICANT: Filiz, Lori
APPLICANT: Neben, Tamlyn
APPLICANT: Whittiers, Mathew
APPLICANT: Wood, Olive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,572
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5853
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1369 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 103..1245
US-08-609-572-3
Query Match 99.4%; Score 1281; DB 1; Length 1369;

Db	1075	TGAGTGTATAACATCTCTGGGAAGTGAAGACCTATCGAAGAAACTTTGCTACGTTTC	1134
Qy	1081	TGGTACCATTGGTTTCACCTTAATATTAGTATATTTGTAAACGGTCTGCTTTTGCGT	1140
Db	1135	TGGTACCATTGGTTTCACCTTAATATTAGTATATTTGTAAACGGTCTGCTTTTGCGT	1134
Qy	1141	AAGCCAACACCTTACCCAAATATGATTCAGATTTTCTGTGATACATGAAGACTTCC	1200
Db	1195	AAGCCAACACCTTACCCAAATATGATTCAGATTTTCTGTGATACATGAAGACTTCC	1254
Qy	1201	ATATCAAGACATGATGATTTGACTCAACAGTTTCCAGTGTATGGCCAAATGTTCAATATGA	1260
Db	1255	ATATCAAGACATGATGATTTGACTCAACAGTTTCCAGTGTATGGCCAAATGTTCAATATGA	1314
Qy	1261	GTCATCAATAACTGAATTTTCTTTGGAA	1289
Db	1315	GTCATCAATAACTGAATTTTCTTTGGAA	1343

Country	Percentage (%)
Japan	19
Germany	17
Italy	16
France	15
Canada	13
United States	12

Query Match	47.48;	Score 610.4;	DB 1;	Length 1525;	..
Best Local Similarity	70.58;	Pred. No. 1.3e-167;			
Matches 895; Conservative	0;	Mismatches 351;	Indels 24;	Gaps 5	